

PATENT  
USSN 08/974,584  
015389-002950US  
018/206p2

**APPENDIX B****BEST AVAILABLE COPY****Human TERT protein sequence**

LOCUS 014746 1132 aa linear PRI 15-JUN-2002  
DEFINITION Telomerase reverse transcriptase (Telomerase catalytic subunit)  
ORGANISM Homo sapiens  
AUTHORS Nakamura,T.M., Morin,G.B., Chapman,K.B., Weinrich,S.L.,  
Andrews,W.H., Lingner,J., Harley,C.B. and Cech,T.R.  
TITLE Telomerase catalytic subunit homologs from fission yeast and human  
JOURNAL Science 277 (5328), 955-959 (1997)

```
1 mprapr crav rsllrshyre vlplatfvrr lgpqgwrlvq rgdpaafraI vaqclvcvpw
61 darpppaaps frqvscikel varvlqrIce rgaknvlaIq falldgargg ppeafttsvr
121 sylpntvtda lrgsgawgll lrrvgddvlv hllarcalfv lvapscayqv cgpplyqlga
181 atqarpppha sgprrrlgce rawnhsvrea gvpIglpapg arrrggsasr slpIpkrrpr
241 gaapepertp vggqswahpg rtrgpsdrgr cvvsparpae eatslegals gtrhshpsvg
301 rqhahagpst srpprpwdtp cppvyaetkh flyssgdkeq lrpsfllssl rpsltgarrl
361 vetiflgsrp wmpgtprrlp rlpqrywqmr plflellgnh aqcpygvllk thcplraavt
421 paagvcarek pqgsvaapee edtdprrlvq llrqhsspwq vygfvracIr rlvppglwgs
481 rhnerrflrn tkkfislghk aklsIqeltw kmsvrdcawI rrspgvgcvp aaehrIreeI
541 lakflhwImS vyvvellrsf fyvtettfQk nrIfyrksv wsklqsIgr qhlkrvqlre
601 lseaevrqhr earpalltsr lrfIpkpdgl rplvnmIyv v gartfrrekr aerltsrvka
661 lfsvlnyera rrpqllgasv lglddihrav rtfvlrvraq dpppelyfvk vdvTgaydtI
721 pQdrItevia sllkpqntyc vrryavvqka ahghvrkafk shvstltdlQ pymrqfvahI
781 qetsplrdav vieqssslne assglfdvfl rfmchhavri rgksyvqcqg ipqgsilstI
841 lcsIcygdme nkIfaglrnd glIlrlvddf llvtphltha ktflrtlvrg vpeygcvvnl
901 rktvnfpve dealggtafv qmpahglfpw cgllldtrtl evqsdysya rtsirasltf
961 nrgfkagrnM rrrklfgvlrl kchslfidlQ vnsIqtvcIn Iykilllqay rfhacvlqlp
1021 fhqqvwnkpt fflrvisdta slcysIlkak nagmslgakg aagplpseav qwlchqafll
1081 kltrhrvtYv pllgslrtaq tqIsrkIpgt tltaIeaaan palpsdfkti Id
```

## BEST AVAILABLE COPY



## Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.13 [Nov-27-2005]

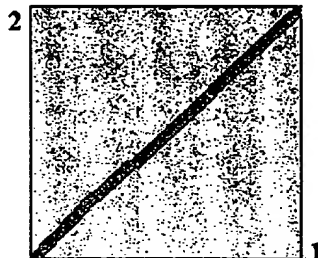
Matrix **BLOSUM62** gap open: **11** gap extension: **1**x\_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☐ View option **Standard**Masking character option **X for protein, n for nucleotide** Masking color option **Black**☐ Show CDS translation

Sequence 1: lcl|seq\_1

Length = 1132 (1 .. 1132)

Sequence 2: lcl|seq\_2

Length = 1122 (1 .. 1122)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

Score = 1340 bits (3468), Expect = 0.0

Identities = 715/1146 (62%), Positives = 839/1146 (73%), Gaps = 38/1146 (3%)

Query	1	MPRAPRCRAVRSLLRSHYREVLPLATFVRRIGPQGWRILVQRGDPAAFRALVAQCLVCVPW	60
		M RAPRC AVRSLRS YREV PLATFVRRIGP+G RLVQ GDP +R LVAQCLVC+ W	
Sbjct	1	MTRAPRCFAVRSLLRSRYREVWPLATFVRRIGPEGRRILVQPGDPKIYRTLVAQCLVCMHW	60
Query	61	DARPPPAAPSFQVSCLELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR	120
		++PPPA SF QVS LKELVARV+QRLCER +NVLAFGF LL+ ARGGPP AFT+SVR	
Sbjct	61	GSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR	120
Query	121	SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA	180
		SYLPNTV + LR SGAW LLL RVGDD+LV+LLA CAL++LV PSCAYQVCG PLYQ+ A	
Sbjct	121	SYLPNTVIETLRVSGAWMLLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA	180
Query	181	ATQARPPPHAS-GPRRRLG-----CERAWNHSVREAGVPLGLPAPGARRRGGSASRS	231
		T P AS P R +G ++ + S +EA PL LP+ G +R S S	
Sbjct	181	TTDIWPSVSASYPTRPVGRNFTNLRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTS	240

Query 232 LPLPKRPRRGAAPEPERTFVGQGSWAHPGRTRGPSDRGFCVVSPARP-AEEATSLEGALS 290  
+P K+ R P E P Q G++ PS SP P AE+ S +G +S  
Sbjct 241 VPSAKKARCYPVPRVEEGPHRQVLPTPSGKSWVSPAR----SPEVPTAEKDLSSKGKVS 296

Query 291 GTRHSHPSVGRQHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGD-KEQLRPSFLLSS 349  
S SV +H S PPR P + ET+HFLYS GD +E+L PSFLLS+  
Sbjct 297 DLSLSG-SVCKCHKPSSTSLSPPRQNAFQLRP-FIETRHFYLSRGDQERLNPSFLLSN 354

Query 350 LRPSLTGARRLVETIFLGSRPWMPGTTPRRLPRLPQRYWQMRPLFLELLGNHAQCYPGVLL 409  
L+P+LTGARRLVE IFLGSRP G R RL +RYWQMRPLF +LL NHA+C Y LL  
Sbjct 355 LQPNLTGARRLVEIIFLGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQYVRLL 414

Query 410 KTHCPLRAAVTPAAGVCAREKPOGSVAAPEEEDTDPRLVQLLRQHSSPWQVYGFVRACL 469  
++HC R A + + +T P L+ LLR HSSPWQVYGF+RACL  
Sbjct 415 RSHCRFRTA-----NQQVTDALNTSPPHLMDLLRLHSSPWQVYGFRLACL 459

Query 470 RRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRSPGVGCV 529  
++V LWG+RHNERRF +N KKFISLGK+ KLSLQEL WKM V DC WLR SPG V  
Sbjct 460 CKVVSASLWGRHNERRFFKNLKKFISLGKYGKLSLQELMWKMKVEDCHWLRSPPGKDRV 519

Query 530 PAAEHLREEILAKFLHWMVSVYVVELLSFFYVTETTFQKNRFFYRKSVWSKLQSIGI 589  
PAAEHLRE ILA FL WLM YVV+LLRSFFY+TE+TFQKNRFFYRKSVWSKLQSIG+  
Sbjct 520 PAAEHLRERILATFLFWLMDTYVVQLLSFFYITESTFQKNRFFYRKSVWSKLQSIGV 579

Query 590 RQHLKRVQLRELSAEVRQHREARPALLSRLRFIPKPDGLRPIVNM DYVVGARTFRREK 649  
RQHL+RV+LRELS+ EVR H++ A+ RLRFPKP+GLRPIVNM Y +G R R K  
Sbjct 580 RQHLEVRVRLRELSQEEVRHHQDTWLAMPICRLRFIPKPNGLRPIVNMSYSMGTRALGRRK 639

Query 650 RAERLTSRVKALFVSVLNYERARRPGLLGASVLGLDDIHRWRTFVLRVRAQDPPPELYFV 709  
+A+ T R+K LFS+LNYER + P L+G+SVLG++DI+R WR FVLRVRA D P +YFV  
Sbjct 640 QAQHFTQRLKTLFMSLNYERTKHPHLMGSSVLGMNDIYRTWRAFLRVRALDQTPRMYFV 699

Query 710 KVDVTGAYDTIPQDRLTEVIASIIK-PQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTD 768  
K DVTGAYD IPQ +L EV+A++I+ ++TYC+R+YAVV++ + G V K+F+ V+TL+D  
Sbjct 700 KADVTGAYDAIPQGLVEVVANMIRHSESTYCIQYAVVRRDSQQQVHKSFRRQVTTLS D 759

Query 769 LQPYMRQFVAHLQET--SPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYV 826  
LQPYM QF+ HLQ++ S LR++VVIEQS S+NE+SS LFD FL F+ H V+I + Y  
Sbjct 760 LQPYMGQFLKHLQDSDASALRNSVVIEQSISMNESSSLFDFFLHFLRHSVVKIGDRCYT 819

Query 827 QCQGIPOGSILSTLLCSLCYGMENKLFAGIRRDGLLLRLVODFLLVTPHLTHAKTFLRT 886  
QCQGIPOGS LSTLLCSLC+GDMENKLFA ++RDGLLLR VDDFLLVTPHL AKTFL T  
Sbjct 820 QCQGIPOGSSLSTLLCSLCFGDMENKLF AEVQRDGLLLRFVDDFLLVTPHL DQAKTFLST 879

Query 887 LVRGVPEYGCVVNLKTVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDY 946  
LV GVPEYGC++NL+KTVNFPVE LGG A Q+PAH LFPWCGLLLD+TLEV DY  
Sbjct 880 LVHGVPEYGCMINLQKTVNFPVEPGTLGGAAPYQLPAHCLFPWCGLLLDQTLEVFCDY 939

Query 947 SSYARTSIRASLTFNRGFKAGRNMRRKLFGLRLKCHSLFLDLQVNSLQTVCTNIYKILL 1006  
S YA+TSI+ SLTF FKAG+ MR KL VLRLKCH LFLDLQVNSLQTV C NIYKI L  
Sbjct 940 SGYAQTSIKTSLTFQSVFKAGKTMRNKLLSVLRLKCHGLFLDLQVNSLQTV CINIYKIFL 999

Query 1007 LQAYRFHACVLQLPFHQVWKNPTFFLRLVISDTASLCYSILKAKNAGMSLGAKGAAGPLP 1066  
LQAYRFHACV+QLPF Q+V KN TFFL +IS AS CY+ILK KN GM+L A G+ P  
Sbjct 1000 LQAYRFHACVIQLPFDQVRKNLTFFLGISSQASCCYAILKVNPGMTLKASGS---FP 1056

Query 1067 SEAVQWLCHQAFLKLTRHRVTVYVPLLSLRTAQTLRSRKLPGTTLTALEAAANPALPSD 1126  
EA WLC+QAFLLKL H V Y LLG LRTAQ L RKLP T+T L+AAA+PAL +D  
Sbjct 1057 PEAHWLCYQAFLKLAAHSVYIKCLLGPLRTAQKLLCRKLPEATMTILKAAADPALSTD 1116

Query 1127 FKTILD 1132  
F+TILD  
Sbjct 1117 FQTILD 1122

CPU time: 0.07 user secs. 0.00 sys. secs 0.07 total secs.

Lambda K H  
0.324 0.138 0.434

Gapped  
Lambda K H  
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 9278

Number of extensions: 5864

Number of successful extensions: 8

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 1132

Length of database: 1,129,354,045

Length adjustment: 144

Effective length of query: 988

Effective length of database: 1,129,353,901

Effective search space: 1115801654188

Effective search space used: 1115801654188

Neighboring words threshold: 9

X1: 15 ( 7.0 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 40 (21.6 bits)

S2: 84 (37.0 bits)